

THAT WHICH IS CLAIMED:

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1. An isolated nucleotide sequence selected from the group consisting of:
- a) a nucleotide sequence encoding a plant GDP-mannose pyrophosphorylase;
  - b) a nucleotide sequence encoding the amino acid sequence of
- 5 SEQ ID NO:2;
- c) a nucleotide sequence set forth in SEQ ID NO:1;
  - d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1;
  - e) a nucleotide sequence having at least 90% identity to a
- 10 nucleotide sequence of a), b), c) or d);
- f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and
  - g) a nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f); and fragments and variants thereof.

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~~2. The isolated nucleotide sequence of claim 1, wherein said GDP-mannose pyrophosphorylase is native to maize or a leguminous plant.~~

3. The isolated nucleotide sequence of claim 2, wherein said GDP-mannose is native to maize.

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4. The isolated nucleotide sequence of claim 2, wherein said leguminous plant is selected from the group consisting of beans and peas.

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5. An expression cassette comprising a nucleotide sequence of claim 1, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.

6. The expression cassette of claim 5, wherein said GDP-mannose pyrophosphorylase is native to maize or a leguminous plant.

5 7. The expression cassette of claim 6, wherein said GDP-mannose pyrophosphorylase is native to maize.

SUB C3 8. The expression cassette of claim 6, wherein said leguminous plant is selected from the group consisting of beans and peas.

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9. The expression cassette of claim 5, wherein said promoter is a tissue-specific promoter.

10. The expression cassette of claim 9, wherein said promoter is a seed-preferred promoter.

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SUB B 11. The expression cassette of claim 10, wherein said promoter is selected from the group of promoters consisting of: cim1, cZ19B1, celA, gama-zein, glob-1 and phaseolin.

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12. The expression cassette of claim 5, wherein said promoter is a constitutive promoter.

13. The expression cassette of claim 12, wherein said promoter is a ubiquitin or a Scp1 promoter.

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14. A method for over-expressing GDP-mannose in a plant, comprising:  
a) transforming a plant cell with at least one nucleotide sequence encoding a GDP-mannose pyrophosphorylase, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant;  
b) screening the plant cells transformed in step (a) for stable expression of GDP-pyrophosphorylase to obtain positive cultures;  
c) regenerating said positive cultures into a plant; and  
d) growing the plant from step (c) under conditions appropriate for synthesis of said GDP-mannose.

15. The method of claim 14, wherein said nucleotide sequence is selected from the group consisting of:  
a) a nucleotide sequence encoding a GDP-mannose pyrophosphorylase that is native to maize or a leguminous plant;  
b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;  
c) a nucleotide sequence set forth in SEQ ID NO:1;  
d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1; and  
e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d);  
f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and

16. The method of claim 15, wherein said GDP-mannose pyrophosphorylase is native to maize.

17. The method of claim 15, wherein said leguminous plant is selected from the group consisting of beans and peas.

18. The method of claim 15, wherein said promoter is a constitutive promoter.
19. The method of claim 18, wherein said promoter is a ubiquitin or a Scp1 promoter.
20. The method of claim 15, wherein said promoter is a tissue-specific promoter.
21. The method of claim 20, wherein said promoter is a seed-preferred promoter.
22. The method of claim 21, wherein said promoter is from the group of promoters consisting of: cim1, cZ19B1, celA, gama-zein, glob-1 and phaseolin.
23. A recombinant plant cell having stably incorporated into its genome at least one nucleotide sequence encoding a GDP-mannose pyrophosphorylase or an antisense RNA thereof; wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.
24. The plant cell of claim 23, wherein said nucleotide sequence is selected from the group consisting of:
- a) a nucleotide sequence encoding a GDP-mannose pyrophosphorylase that is native to maize or a leguminous plant;
  - b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;
  - c) a nucleotide sequence set forth in SEQ ID NO:1;
  - d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1;
  - e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d);

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f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and

g) a nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f); and fragments and variants thereof.

25. The plant cell of claim 24, wherein said GDP-mannose pyrophosphorylase is native to maize.

10 26. The plant cell of claim 24, wherein said leguminous plant is selected from the group consisting of beans and peas.

27. The plant cell of claim 24, wherein said promoter is a constitutive promoter.

15 28. The plant cell of claim 27, wherein said promoter is a ubiquitin or a Scp1 promoter.

29. The plant cell of claim 24, wherein said promoter is a tissue-specific promoter.

20 30. The plant cell of claim 29, wherein said promoter is a seed-preferred promoter.

25 31. The plant cell of claim 30, wherein said promoter is selected from the group of promoters consisting of: cim1, cZ19B1, celA, gama-zein, glob-1 and phaseolin.

30 32. A transformed plant having stably incorporated into its genome at least one nucleotide sequence encoding a GDP-mannose pyrophosphorylase or an antisense sequence thereof; said sequence operably linked to a promoter that drives expression in a plant.

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33. The plant of claim 32, wherein said nucleotide sequence is selected from the group consisting of:
- a) a nucleotide sequence encoding a GDP-mannose pyrophosphorylase that is native to maize or a leguminous plant;
  - b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;
  - c) a nucleotide sequence set forth in SEQ ID NO:1;
  - d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1;
  - e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d);
  - f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and
  - g) a nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f); and fragments and variants thereof.
34. The plant of claim 33, wherein said GDP-mannose pyrophosphorylase is native to maize.
35. The plant of claim 33, wherein said leguminous plant is selected from the group consisting of beans and peas.
36. The plant of claim 33, wherein said promoter is a constitutive promoter.
37. The plant of claim 36, wherein said promoter is a ubiquitin or a Scp1 promoter.
38. The plant of claim 33, wherein said promoter is a tissue-specific promoter.

39. The plant of claim 38, wherein said promoter is a seed-preferred promoter.

5 40. The plant of claim 39, wherein said promoter is selected from the group of promoters consisting of: cim1, cZ19B1, celA, gama-zein, glob-1 and phaseolin.

10 41. The plant of <sup>claim 32</sup> ~~any of claims 32-40~~, wherein said plant is a monocot.

42. The plant of claim <sup>32</sup> ~~41~~, wherein said monocot is maize, wheat, rice, barley, sorghum, or rye.

15 43. The plant of <sup>claim 32</sup> ~~any of claims 32-40~~, wherein said plant is a dicot.

44. The plant of claim <sup>32</sup> ~~43~~, wherein said dicot is soybean, Brassica, sunflower, alfalfa, or safflower.

<sup>Sub 32</sup> 20 45. The seed of the plant of claim <sup>32</sup> ~~41~~.

46. The seed of the plant of claim 42.

47. The seed of the plant of claim 43.

25 48. The seed of the plant of claim 44.

30 49. A method for down-regulating the expression of GDP-mannose pyrophosphorylase, comprising: transforming a plant cell with a least one nucleotide sequence encoding an antisense RNA to a GDP-mannose pyrophosphorylase RNA, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.

50. The method of claim 49, wherein said GDP-mannose pyrophosphorylase RNA is selected for the group consisting of:

- a) a nucleotide sequence encoding a GDP-mannose pyrophosphorylase that is native to maize or a leguminous plant;
- b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;
- c) a nucleotide sequence set forth in SEQ ID NO:1;
- d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1; and
- e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d);
- f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and
- g) a nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f) ;and fragments and variants thereof.

51. The method of claim 50, wherein said GDP-mannose pyrophosphorylase is native to maize.

52. The method of claim 50, wherein said leguminous plant is selected from the group consisting of beans and peas.

53. The method of claim 49, wherein said promoter is inducible or developmentally regulated.

54. The method of claim 53, wherein said promoter is tissue-specific.

55. The method of claim 54, wherein said promoter is tassel-specific.



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56. A method for manipulating gum production in a plant of interest, comprising the steps of:

- a) transforming plant cells with at least one nucleic acid sequence encoding an enzyme in a galactomannan biosynthetic pathway or an antisense RNA thereto; wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant;
- b) screening the plant cells transformed in step (a) for stable expression of said enzyme or said antisense RNA to obtain positive cultures;
- c) regenerating said positive cultures into a plant; and
- d) growing the plant from step (c).

57. The method of claim 56, wherein said manipulating up-regulates gum production.

58. The method of claim 56, wherein said manipulating down-regulates gum production.

59. The method of claim 56, wherein said enzyme is selected from the group consisting of: GDP-mannose pyrophosphorylase, mannan synthase and galactosyl transferase.

60. The method of claim 59, wherein said enzyme is GDP-mannose pyrophosphorylase.

61. The method of claims 56-60, wherein said plant of interest is a monocot.

62. The method of claim 61, wherein said monocot is maize, wheat, rice, barley, sorghum, or rye.

63. The method of claims 56-60, wherein said plant of interest is a dicot.

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64. The method of claim 63, wherein said dicot is soybean, Brassica, sunflower, alfalfa or safflower.

5 65. A recombinant plant cell having stably incorporated into its genome at least one nucleic acid sequence encoding an enzyme in a galactomannan biosynthetic pathway or an antisense RNA to an enzyme in a galactomannan synthetic pathway; wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.

10 66. A transformed plant having stably incorporated into its genome at least one nucleic acid sequence encoding an enzyme in a galactomannan biosynthetic pathway or an antisense RNA to an enzyme in a galactomannan synthetic pathway; wherein said nucleotide sequence is operably linked to a heterologous promoter that drives expression in a plant cell.

15 67. The transformed plant of claim 66, wherein said transformed plant is a monocot.

20 68. The transformed plant of claim 67, wherein said plant is maize, wheat, rice, barley, sorghum or rye.

69. The transformed plant of claim 66, wherein said plant is a dicot.

25 70. The transformed plant of claim 69, wherein said dicot is soybean, Brassica, sunflower, alfalfa or safflower.

71. A recombinant protein encoded by nucleotide sequences selected from the group consisting of:

- a) a nucleotide sequence encoding a GDP-mannose pyrophosphorylase;
- 5 b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;
- c) a nucleotide sequence set forth in SEQ ID NO:1;
- d) a nucleotide sequence comprising at least 20 contiguous nucleotides of SEQ ID NO:1;
- 10 e) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), c) or d);
- f) a nucleotide sequence that hybridizes to a nucleotide sequence of a), b), c), d) or e) under stringent conditions; and
- 15 g) a nucleotide sequence encoding an antisense RNA of a nucleotide sequence of a), b), c), d), e) or f); and fragments and variants thereof.

72. The recombinant protein of claim 71, wherein said GDP-mannose pyrophosphorylase is native to maize.

20 *sub B7* 73. Variants of the recombinant protein of claim 72.

74. A method for down-regulating levels of GDP-mannose by cosuppression, comprising transforming a plant cell GDP-mannose pyrophosphorylase with at least one nucleotide sequence encoding a truncated  
25 enzyme of a GDP-mannose biosynthetic pathway; wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.

75. The method of claim 74 wherein said truncated enzyme is a truncated GDP-mannose pyrophosphorylase.

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